## **HLA Ligand/Motif Database**

lymphocytes (T cells) play a crucial role in the body's immune response to infectious disease. They are responsible for activating and participating in the inflammatory response, destroying cells infected with pathogenic microorganisms, and providing help for B cell antibody production. In addition, they contribute to pathogenic immune associated responses with autoimmune diseases and organ transplant rejection. Understanding and controlling the T cell response is an important aspect in the improvement of existing vaccines and development of new broad range vaccines and immunotherapeutics. T cells recognize small peptide fragments derived from endogenous or exogenous proteins, termed ligands, that are presented on antigen presenting molecules, termed HLA in humans. The determination of which ligands elicit the most efficient T cell responses is part of the fundamental knowledge required for rationale design and developvaccines ment of and

immunotherapeutics. The HLA Ligand/Motif Database was conceived in 1999 as part of a NIAID-supported initiative to improve human vaccine efficacy and safety through basic and applied research. This database is maintained by Dr. William Hildebrand at the University of Oklahoma Health Sciences Center, and includes information on both microbe-derived and host-derived HLA peptide ligands.

The HLA Ligand/Motif Database provides a searchable, qualitycontrolled resource to the public via the World Wide Web. Detailed information about a particular ligand includes: investigator and literature sources, ligand description, and the peptide binding motif for the HLA allele. The database website provides user-friendly methods for ligand and motif searches and also accepts the submission of new ligand/motif data from the scientific community. This resource facilitates the sharing of data amongst investigators across

many disciplines and enhances the potential for rationale immunotherapeutic and vaccine design.

To obtain information about specific ligands or to use the HLA binding epitope prediction algorithm, please visit the program's website at: http://hlali gand.ouhsc.edu/LigandDB/ servlet/GenerateFormServl et?form\_type=index. more information about other NIAID biodefense research go resources, please www.niaid.nih.gov/biodefense.





